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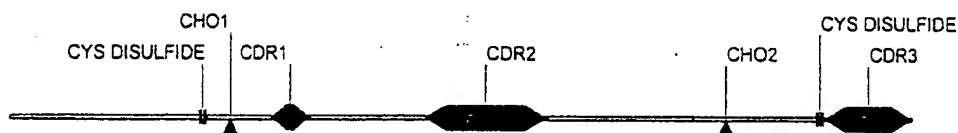
Figure 1. Alignment of Thy-1 and 8E5 VH

| | | | | | |
|-------------------|-------|----------------------------------|-----------|---------------------|---------|
| | | 1 | | | 50 |
| EcFv-1.15* 8E5 VH | (1) | -----QLOQS--G--AELVKPGA | SVKMS | MA | SGYTF |
| Thy1 human | (1) | MNLAISIALLLTVLQVSRGQKVTSLTACLVDO | SLRLD | CRHENT | SSSPIQY |
| Consensus | (1) | QL | SLKL CK | S S | |
| | | 51 | | | 100 |
| EcFv-1.15* 8E5 VH | (33) | HWVKORPGQGLEWIGTIDPADSYTSYNQNF | ----- | ----- | KDKA |
| Thy1 human | (51) | ESSLTRETKKHVLFGTIDGVP | HTYRSRT | NETSKYHMKVLYLSAFTSK | DEG |
| Consensus | (51) | F R GTI D NF | | | KD A |
| | | 101 | | | 150 |
| EcFv-1.15* 8E5 VH | (67) | FLVDPKPSSTAYMQESSLTFGDSAVYFCARE | SYRYFFDY | WGHGTT | TV |
| Thy1 human | (101) | TYTCALHHS | GHSPPISSQ | NVTVLRDKLVKCE | ISLLAQN |
| Consensus | (101) | T T S ISS | EGI | W | LSL |
| | | 151 | 161 | | |
| EcFv-1.15* 8E5 VH | (117) | SSAKTTPKE-- | | | |
| Thy1 human | (151) | SLLOAIDFMSL | | | |
| Consensus | (151) | S T L | | | |

Figure 1B. Design of a single Ig domain CDR binding polypeptide based on the Thy-1 structure.

Qvsrgqkvtsltacldvqslrldcrhentsssnym
Hfsltretkkhvlfgtidpadsytsynqnfkdegtytc
Alhhsghspissqnvtvlrdklvkcegyyryyfdy

Figure 1C. Diagram of a single Ig domain CDR carrier based on the Thy-1 structure.



Thy1/8E4 VH synthetic CDR binding polypeptide
111 aa

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FIGURE 2A

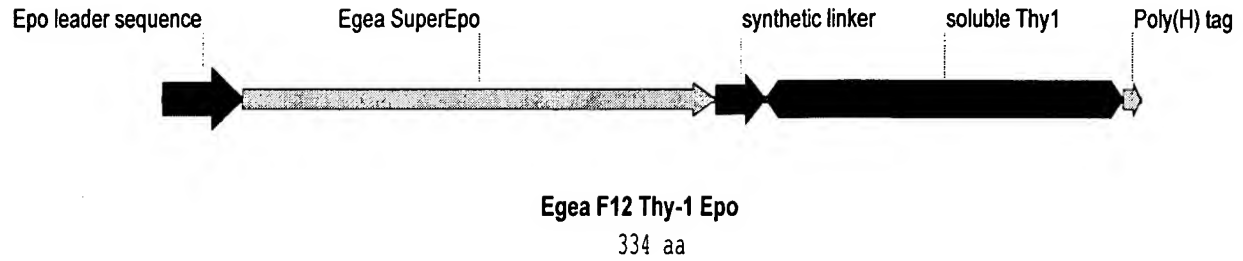


FIGURE 2B

| | | | | | |
|-----|------------|------------|------------|------------|------------|
| 1 | MGVHECPAWL | WLLLSLLSLP | LGLPVLGAPP | RLICDSRVLE | RHLLEAKEAE |
| 51 | SITTGCVEDC | SLNENITVPD | SKVNFYAWKR | MEVGQQAVEV | WQGLALLSEA |
| 101 | VLRGQALLVI | SSQPWEPLQL | HVDKAVSGLR | SLTTLLRALG | AQKEAISPPD |
| 151 | AASAAPLRTI | TADTFRKLFR | VYPNFLRGKL | KFYTGACRG | GGGSGGGGE |
| 201 | FGGGGSQKVT | SLTACLVDQS | LRLDCRHENT | SSSPIQYEFS | LTRETKKHVL |
| 251 | FGTVGVPEHT | YRSRTNFTSK | YHMKVLYLSA | FTSKDEGTYT | CALHHSGHSP |
| 301 | PISSQNVTVL | RDKLVKCEGI | SLLAQNTSHH | HHHH | |

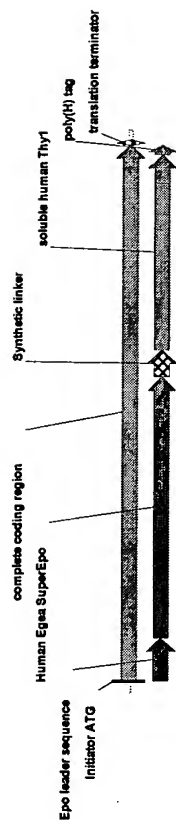
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FIGURE 2C

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HindIII
-----
      M G V H E C P A W L W L L L S L L S L P
1  GATTGGCGAA GCTTGGAGGA ATGGGCGTGC ACGAGTGTCC CGCCTGGCTG TGGCTGCTGC TGAGCCTGCT GAGCCTGTCC
   L G L P V L G A P P R L I C D S R V L E R H L L E A K .
81 CTGGGCTGCT CCGTGTGGG CGCCCCCCCC CGGCTGATCT GCGACAGCCG GGTGCTGGAG CGGCACCTGC TGGAGGCCAA
   . E A E S I T T G C V E D C S L N E N I T V P D S K V N .
161 GGAGGCCGAG AGCATCACCA CCGGCTGCGT GGAGGACTGC AGCCTGAACG AGAACATCAC CGTGCCCGAC AGCAAGGTGA
   . F Y A W K R M E V G Q Q A V E V W Q G L A L L S E A
241 ACTTCTACGC CTGGAAGCGG ATGGAGGTGG GCCAGCAGGC CGTGGAGGTG TGGCAGGGCC TGGCCCTGCT GAGCGAGGCC
   V L R G Q A L L V I S S Q P W E P L Q L H V D K A V S .
321 GTGCTGCGGG GCGAGGCCCT GCTGGTGATC AGCAGCCAGC CCTGGGAGCC CCTGCAGCTG CACGTGGACA AGGCCGTGAG
   . G L R S L T T L L R A L G A Q K E A I S P P D A A S A .
401 CCGCCTGCGG AGCCTGACCA CCCTGCTGCG GGCCCTGGGG GCCCAGAAGG AGGCCATCAG CCCCCCGAC GCCGCCAGCG
   . A P L R T I T A D T F R K L F R V Y P N F L R G K L
481 CCGCCCCCT GCGGACCATC ACCGCCGACA CTTCCGGAA GCTGTCCGG GTGTACCCCA ACTTCCTGCG GGGCAAGCTG
   K F Y T G E A C R G G G G G S G G G G E F G G G G S Q .
561 AAGTTCTACA CCGCGAGGC CTGCCGGGGC GCGCGGCGCG GCAGCGGCGG CGGCAGCGAG TTCGGCGGCG GCGGCAGCCA
   . K V T S L T A C L V D Q S L R L D C R H E N T S S S P .
641 GAAGGTGACC AGCCTGACCG CCTGCCTGGT GGACCAGAGC CTGCGGCTGG ACTGCCGGCA CGAGAACACC AGCAGCAGCC
   . I Q Y E F S L T R E T K K H V L F G T V G V P E H T
721 CCATCCAGTA CGAGTTCAGC CTGACCCGGG AGACCAAGAA GCACGTGCTG TTCGGCACCG TGGGCGTGCC CGAGCACACC
   Y R S R T N F T S K Y H M K V L Y L S A F T S K D E G .
801 TACCGGAGCC GGACCAACTT CACCAGCAAG TACCACATGA AGGTGCTGTA CCTGAGCGCC TTCACCAGCA AGGACGAGGG
   . T Y T C A L H H S G H S P P I S S Q N V T V L R D K L .
881 CACCTACACC TGCGCCCTGC ACCACAGCGG CCACAGCCCC CCCATCAGCA GCCAGAACGT GACCGTGCTG CGGGACAAGC
                                     BamHI
                                     ~~~~~
   . V K C E G I S L L A Q N T S H H H H H H * * *
961 TGGTGAAGTG CGAGGGCATC AGCCTGTGTT CCCAGAACAC CAGCCACCAC CACCACCACC ACTGATGATA AGATCGGATC
   BamHI
   ~
1041 CTAGGCTTCC
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Epo F12 Thy-1 Epo

1000 bp

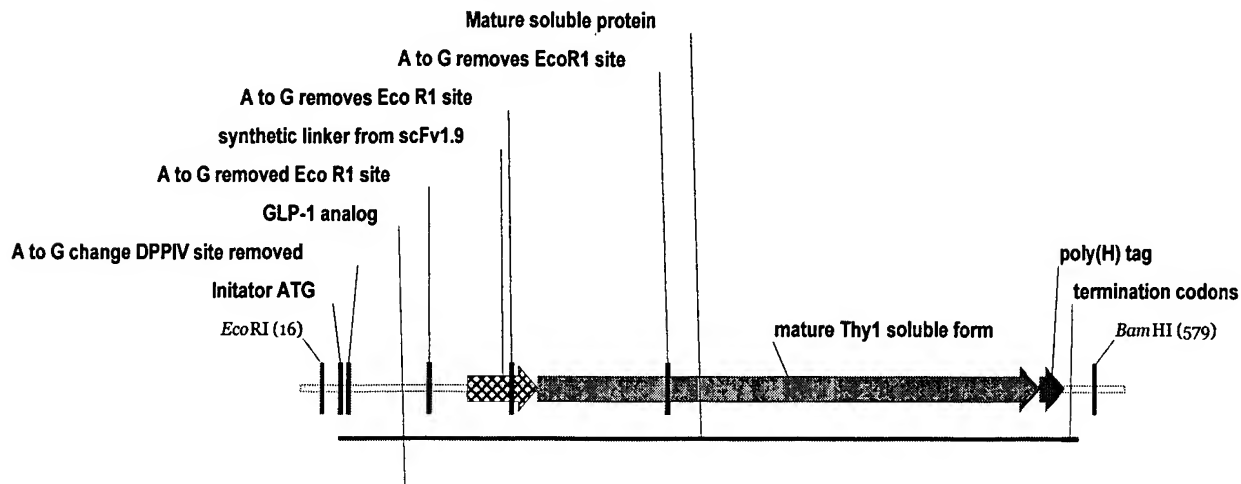
1 GATTGGCGAA GCTTGGAGGA ATGGCGGTG ACAGTGGCC CGCCTGGCTG TGGCTGGCTG TGAGCTGCTG GAGCTGGCC CTGGGCTGCG CCGTGGCTGG
CTAACCGCTT CGAACCTCTT TACCGCCAG TGCTCACGG CGGACCCGAC ACCGACCGAG ACTCGGACGA CTCGGACGGG GACCCGGAGC GGCACGACCC
101 GlyProPro ArgLeuileCys AspSerArg ValLeuGlu ArgHisLeuLeu GluAlaGlu SerLeThrThr GlyCysVal GluAspCys
CGCCCGCCCG CGGTGATCT CGACAGCCG GGTGCTGGAG CGGACCTGC TGGAGGCCAA GGAGCCGAG AGCATCACCA CCGCTGCGT GGAGGACTGC
CGCGGGGGG CGCAGTACA CGCTGTCGG CCAGACCTC GCGTGGAGC ACCTCCGTT CCGCGGCTC TCGTAGTGTG GCGCGACGCA CTCCTGACG
201 SerLeuAsnGlu AsnileThr ValProAsp SerLysValAsn PheTyrAla TrpLysArg MetGluValGly GlnGlnAla ValGluVal TrpGlnGlyLeu
AGCTGAACG AGAATATCAC CGTGCCCGAC AGCAAGTGA ACTTCTAGC CTGGAAGCG ATGAGGTGG GCGACAGGC CTGGAGGTG TGGCAGGGCC
TCGACTTGC TCTTGTAGT GCACGGGTG TCGTTCACCT TGAAGATGCG GACCTTCGCC TACTCCACC CGTCTGTCG GCACCTCCAC ACCGTCCCG
301 LAlaLeuLeu SerGluAla ValLeuArgGly GlnAlaLeu LeuValile SerSerGlnPro TrpGluPro LeuGlnLeu HisValAspLys AlaValSer
TGGCCTGCT GAGCAGGCC GTGTGCGGG GCCAGCCCT GCTGTGATC AGCAGCCAGC CTTGAGGCTG CACCTGAGC CACCTGGACA AGGCCGTGAG
ACCGGGACGA CTCGTCCGG CACGACGCC CGGTCCGGG GACCACTAG TCGTGGTGC GACCTTCGG GAGCTGAG GTGCACCTGT TCCGCGACTC
401 GlyLeuArg SerLeuThrThr LeuLeuArg AlaLeuGly AlaLeuSer ProProAsp AlaAlaSerAla AlaProLeu ArgThrIle
CGGCTGCGG AGCTGACCA CCTGCTGG GGCCTGGG GCCAGAGG AGCCATAG CCCCCCGAC GCGCCCGCTG CCGCCCGCTG CCGCTGGTAG
GCCGACGCC TCGACTGT GGGACGACGC CCGGACCCG CGGTCTTCC TCCGCTAGT GGGGGGGCTG CCGCGGTGC GCGGGGGGA CCGCTGGTAG
501 ThrAlaAspThr PheArgLys LeuPheArg ValTyrProAsn PheLeuArg GlyLysLeu LysPheTyrThr GlyGluAla CysArgGly GlyGlyGlyGly
ACCGCGACA CTTCCGGAA GCTGTCCGG GTGTACCCCA ACTTCTGCG GGGCAAGCTG AGTTCTACA CCGCGAGGC CTGCGGGGG GCGCGCGGG
TGGCGCTGT GGAAGCCTT CGACAAGGC CACATGGGT TGAAGAGC CCGCTTCAG TTCAGATGT GGCCTCCG GACGCCCCG CCGCGCGCG
601 GSerGlyGly GlyGlyGly PheGlyGlyGly GlySerGln LysValThr SerLeuThrAla CysLeuVal AspGlnSer LeuArgLeuAsp CysArgHis
GCAGCGGG CGCGGGGAG TCGCGGGCG GCGGACCCA GAAGTGACC AGCTGACC CCGCTGCTG TCGGACTGCG GAGCGGACCA CCGTGTCTCG GACGCGCGT
CGTCCCGC CCGCGCGCTC AAGCGCGCTC CCGCTCGGT CTTCCACTGG TCGGACTGCG GAGCGGACCA CCGTGTCTCG GACGCGCGT
701 GluAsnThr SerSerSerPro IleGlnTyr GluPheSer LeuThrArgGlu ThrLysLys HisValLeu PheGlyThrVal GlyValPro GluHisThr
CGAGAACC AGCAGCAGCC CCATCCAGTA CGAGTTCAGC CTGACCCGG AGACCAAGAA GCAGTGTCTG TTCGGCACCG TGGCGTGC CGAGCACAC
GCTCTTGTG TCGTGTGCG GTAGGTCTAT GCTCAAGTC GACTGGGCC TCTGTTCTT CGTCACAGC AAGCGTGGC ACCGCGACCG GCTCGTGTG
801 TyrArgSerArg ThrAsnPhe ThrSerLys TyrHisMetLys ValLeuTyr LeuSerAla PheThrSerLys AspGluGly ThrTyrThr CysAlaLeuHis
TACCGAGCC GGACCAACTT CACCAAGAG TACCATGTA AGGTGCTGTA CCGCTGCGG AAGTGTCTG TCCTGCTCC CACCTACAC TGCCTGCTG
ATGCTCTCG CTTGTTTAA GTGTGCTTC ATGTGTACT TCCAGACAT GACTGCGG AGTGTCTG ArgAspLysLeu ValLysCys GluGlyIle SerLeuLeuAla GlnAsnThr
901 HHISerGly HisSerPro ProLeSerSer GlnAsnVal ThrValLeu ArgAspLysLeu ValLysCys GluGlyIle SerLeuLeuAla GlnAsnThr
ACCAAGCG CCACAGCCC CCATCAGCA GCCAGACGT GACCTGTCTG CCGGACAAG TGGTGAAGT GCGAGGCATC AGCTGTCTG CCAAGACAC
TGGTGTGCC GGTGCGGG GGTGTCTG CCGTCTTGA CTGGACGAC GCCCTGTTG ACCACTTCAC GCTCCCGTAG TCGGACGACC GGTCTTGTG
1001 SerHisHis HisHisHisHis
CAGCCACCAC CACCAACC ACTGATGATA AGATCGGATC CTAGCTTCC
GTGCGTGGTG GTGCTGGTGG TGACTACTAT TCTAGCCTAG GATCCGAAG

FIGURE 3

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FIGURE 4A

Egea Thy-1_Glucagon-Like Peptide 1 Non-Immunoglobulin Carrier
Polypeptide



EgeaA42 GLP Thy1 Carrier
600 bp

FIGURE 4B

176 aa

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1  MHGEGTFTSD VSSYLEGQAA KEFIAWLVKG RGGGGGSGGG GEFGGGGSQK
51 VTSLTACLVD QSLRLDCRHE NTSSSPIQYE FSLTRETKKH VLFGTGVGPE
101 HTYRSRTNFT SKYHMKVLYL SAFTSKDEGT YTCALHHS GH SPPISSQNVT
151 VLRDKLVKCE GISLLAQNTS HHHHHH
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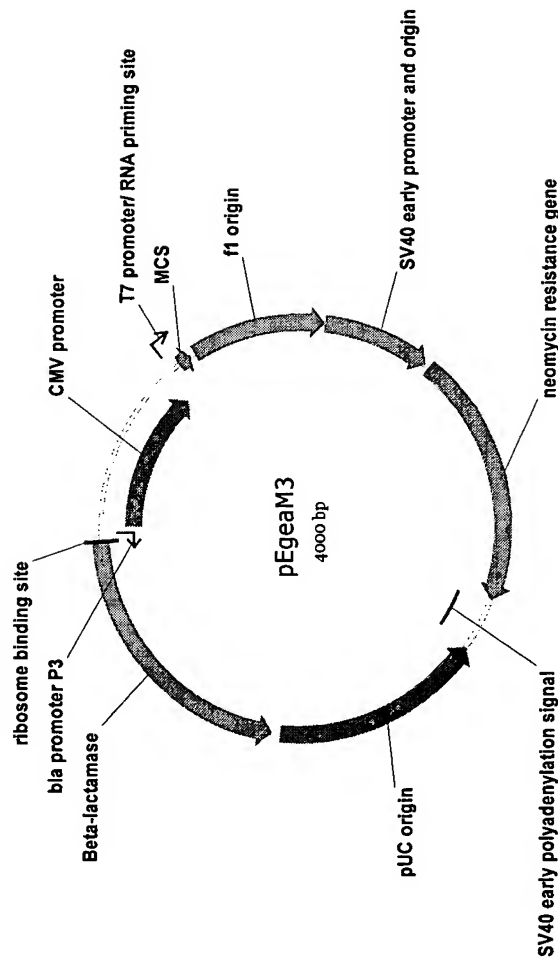
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FIGURE 4C

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                                EcoRI
                                ~~~~~
1      AGTCCGGGAT TTAAGAATTC AGCTGTCCAT GCACGGTGAA GGTACCTTCA CCTCTGACGT TTCTTCTTAC CTGGAAGGTC
      · A A K E F I A W L V K G R G G G G G S G G G G E F G
81     AGGCGGCGAA AGAGTTCATC GCGTGGCTGG TTAAAGGTCG TGGTGGTGGT GGTGGTTCGT GTGGTGGTGG TGAGTTCGGT
      G G G S Q K V T S L T A C L V D Q S L R L D C R H E N ·
161    GGTGGTGGTT CTCAGAAAGT TACCTCTCTG ACCGCGTGCC TGGTTGACCA GTCTCTGCGT CTGGACTGCC GTCACGAAAA
      · T S S S P I Q Y E F S L T R E T K K H V L F G T V G V ·
241    CACCTCTTCT TCTCCGATCC AGTACGAGTT CTCTCTGACC CGTGAAACCA AAAACACGT TCTGTTTCGGT ACCGTTGGTG
      · P E H T Y R S R T N F T S K Y H M K V L Y L S A F T
321    TTCCGGAACA CACCTACCGT TCTCGTACCA ACTTCACCTC TAAATACCAC ATGAAAGTTC TGTACCTGTC TGCCTTCACC
      S K D E G T Y T C A L H H S G H S P P I S S Q N V T V ·
401    TCTAAAGACG AAGGTACCTA CACCTGCGCG CTGCACCACT CTGGTCACTC TCCGCCGATC TCTTCTCAGA ACGTTACCGT
      · L R D K L V K C E G I S L L A Q N T S H H H H H H * * ·
481    TCTGCGTGAC AAAC TGTTA AATGCGAAGG TATCTCTCTG CTGGCGCAGA ACACCTCTCA CCACCACCAC CACCACTGAT
                                BamHI
                                ~~~~~
      · *
561    AATGAGATCT TGAGGCCGGA TCCGCTTAAG ATCCCGGCAA
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| | | | | | | | | | | |
|-----|------------|------------|-------------|------------|------------|------------|------------|------------|-------------|------------|
| 1 | GATTATTCTA | GACCGCGGTT | ACATAACTTA | CGGTAAATGG | CCGCGCTGGC | TGACCGCCCA | ACGACCCCCG | CCCATTTGAC | TCAATAATGA | CGTATGTTCC |
| 101 | CTAATAAGAT | CTGGGCGCAA | TGTATTGAAT | GCCATTACG | GGGGGACCG | ACTGGCGGGT | TGCTGGGGGC | GGGTAACTGC | AGTTATTACT | GCATACAAGG |
| 201 | CATAGTAACG | CCAATAGGGA | CTTTCATTTG | ACGTCAATGG | GTGGAGTATT | TACGGTAAAC | TGCCCACTTG | GCAGTACATC | AAGTGATATCA | TATGCCAAGT |
| 301 | GTATCATTGC | GGTTATCCCT | GAAAGGTAAAC | TGCAGTTACC | CACCTCATAA | ATGCCATTAG | ACGGGTGAAC | CGTCATGTAG | TTCACATAGT | ATACGGTTCA |
| 401 | ACGCCCCCTA | TTGAGGTCAA | TGACGGTAAA | TGGCCCGCCT | GGCATTATGC | CCAGTACATG | ACCTTATGGG | ACTTTCCTAC | TTGGCAGTAC | ATCTACGTAT |
| 501 | TGCGGGGGAT | AATGTCAGTT | ACTGCCATTT | ACCGGCGGGA | CCGTAATACG | GGTCATGTAC | TGGAATACCC | TGAAAGGATG | AACCGTCAATG | TAGATGCATA |
| 601 | TAGTCATCGC | TATTACCATG | GTGATGCGGT | TTTGGCAGTA | CATCAATGGG | CGTGGATAGC | GGTTTGACTC | ACGGGGATTI | CCAAGTCTCC | ACCCATTGA |
| 701 | ATCAGTAGCG | ATAATGGTAC | CACATACGCCA | AAACCGTCAI | GTAGTTACCC | GCACCTATCG | CCAAACTGAG | TGCCCTTAAA | GGTTCAGAGG | TGGGGTAACT |
| 801 | CGTCAATGGG | AGTTTGTGTT | GGCACCAAAA | TCAACGGGAC | TTTCCAAAT | GTGCTAACAA | CTCGCCCCCA | TTGACGCCAA | TGGCGGGTAG | GGGTGTACGG |
| 901 | GCAGTTACCC | TCAACAAAA | CCGTGGTTTT | AGTTGCCCTG | AAAGGTTTTA | CAGCATTTGT | GAGCGGGGT | AACTGCGGTT | ACCGCCCATC | CGCACATGCC |
| | TGGGAGGTCT | ATATAAGCAG | AGCTCTCTGG | CTAAGTAGAA | TGCAATTTAA | TAGACTCAC | TATAGGGAGA | CCCAAGCTGG | CTAGCGTTTA | AACTTAAGCT |
| | ACCTCCAGA | TATATTGTC | TCGAGAGACC | GATTGATCTT | AGCTTTAATT | ATGCTGAGTG | ATATCCCTCT | GGGTTGACCC | GATCGCAAAI | TTGAATTGCA |
| | TGGTACCGAG | CTCGGATCCA | CTCTAGGGGG | TATCCCAAG | CGCCCTGTAG | CGGCGCATTA | AGCGGGCGGG | GTGTGGTGGT | TACGCGCAGC | GTGACCGCTA |
| | ACCATGGCTC | GAGCTTAGGT | GAGATCCCCC | ATAGGGGTGC | GCGGGACATC | GCCCGGTAAT | TCCGCGGCTT | TCCCGGTCAA | GCTCTAAATC | CACTGGCGAT |
| | CACTTGCCAG | CGCCCTAGCG | CCCGTCCCTT | TGCGTCTCTT | CCCTTCTCTT | CTCGCCACGT | TGCGCGGCTT | AGGGGCGGAA | CGAGATTTAG | GGGGGCTCCC |
| | GTGAACGGTC | GCGGGATCGC | GGGGAAGGAA | AGCGGAGGAA | GAGCGGTGCA | AGCGGCGGAA | AGGGGCGGTT | CGAGATTTAG | CGCCCTGATA | GACGGTTTTT |
| | TTTAGGGTTC | CGATTAGTG | CTTTAGGGCA | CCTCGACCCC | AAAAACTTG | ATTAGGGTGA | TGGTTCAGCT | AGTGGGCCAT | CGCCCTGATA | GACGGTTTTT |
| | AAATCCCAAG | GCTAAATCAC | GAAATGCCGT | GGAGCTGGGG | TTTTTTGAAC | TAATCCCACT | ACCAAGTGCA | TCACCCGGTA | GCGGGACTAT | CTGCCAAAAA |
| | CGCCCTTTGA | CGTTGGAGTC | CACGTTCTTT | AATAGTGAGC | TCTTGTCCA | AACTGGAACA | ACACTCAAC | CTATCTCGGT | CTATCTTTT | GATTTATAG |
| | GCGGAAACT | GCAACCTCAG | GTGCAAGAAA | TTATCACCTG | AGAACAAAGT | TTGACCTTGT | TGTGAGTTGG | GATAGAGCCA | GATAAGAAAA | CTAAATATTC |

FIGURE 5

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1001 GGATTCTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTAATT CTGTGGAATG TGTGTCAATT AGGTGTGGA
1101 CCTAAACGG CTAAGCCCG ATAAACAAIT TTTTACTCGA ATGCAAAAGC TGCACTCTCA TTAGTCAGCA ACCAGGTGTG GACACTTTAC ACACAGTCAA TCCACACCT
1201 AAGTCCCCAG GCTCCCCAGC AGGCAAGAAT ATGCAAAAGC TACGTTTCGT TACGTTTCGT TACGTTTCGT TACGTTTCGT TACGTTTCGT TACGTTTCGT TACGTTTCGT
1301 GTATGCAAGC CATGATCTC AATTAGTTCG TTAATCAGTC AGAGCCGAG TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC
1401 AATGAGTTC CTAATTTTTT TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG TTAATTTATG
1501 GGTACCGACT GATTAAAGAA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA TCGTTTCGCA
1601 AAAAGCTTTT TCGAGTCTCT AGCAATCGCT ACTAATCTGT TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC TCGTTCGCTC
1701 GGCAACAACG ACAATCGCT GCTCTGATG CCGCTGATG CCGCTGATG CCGCTGATG CCGCTGATG CCGCTGATG CCGCTGATG CCGCTGATG CCGCTGATG
1801 TACTTTGAC TCCTGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG TCGGCTCCG
1901 CCGAGTAAI CCCGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC
2001 ATGCAACTG AGCATCAGG GCTCGCGCA GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC GCGGCTTAC
2101 GACTGCTTC TCGTAGTCCG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG TGGAATCATG
2201 GGACGAACGG CTTATAGTAC CACTTTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC CCGGCTTAC
2301 TACCGTGTAT ATTGCTGAAG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG AGCTTGGCG
2401 CGCTTCTTG TAACGACTTC TCGAACCGCC CACTTGGCG CACTTGGCG CACTTGGCG CACTTGGCG CACTTGGCG CACTTGGCG CACTTGGCG CACTTGGCG
2501 GCGGAAGAAC TGCTCAAGAA GACTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT TGCTCGCCCT
2601 TAAGCATTT TTTTCACTG ATTCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT TGCTAGTT
2701 AAGSCCAGCA AAAGCCAGG AACGTAAAC AACGTAAAC AACGTAAAC AACGTAAAC AACGTAAAC AACGTAAAC AACGTAAAC AACGTAAAC
2801 TCAGAGTGG CGAAACCCG CAGGACTATA AAGTACCAG CCGTTCCCG CCGTTCCCG CCGTTCCCG CCGTTCCCG CCGTTCCCG CCGTTCCCG CCGTTCCCG
2901 AGTCTCCAC GCTTTGGGT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT GTCTGTGAT
3001 ATGACACAGG GGAAGAGGG AAGGCTTCCG CAGCGCGAA CAGCGCGAA CAGCGCGAA CAGCGCGAA CAGCGCGAA CAGCGCGAA CAGCGCGAA CAGCGCGAA
3101 GTGTGCAGCA ACCCCCGGT CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC CAGCCCGAC
3201 AGCCACTGTT AACAGGATTA GCAGAGCGAG GTATGTAGG GTATGTAGG GTATGTAGG GTATGTAGG GTATGTAGG GTATGTAGG GTATGTAGG GTATGTAGG
3301 TCGGTGACCA TTGTCTTAAT CGTCTCGTC CAYACATCG CAYACATCG CAYACATCG CAYACATCG CAYACATCG CAYACATCG CAYACATCG CAYACATCG
3401 GGATCTGCG CTCTGCTGAA GCGATTACC TCGGAAAAA GAGTTGGTAG CTCTGATCC CTCTGATCC CTCTGATCC CTCTGATCC CTCTGATCC CTCTGATCC
3501 CCAATAGACG GAGACGACTT CGTCAATAGT AAGCTTTT CACTCAACAT CACTCAACAT CACTCAACAT CACTCAACAT CACTCAACAT CACTCAACAT CACTCAACAT
3601 AGCAGCAGAT TACGCGCAGA AAAAAGGAT CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG CTCAGAAAG
3701 TCGTCTGCTA ATGCGCGTCT TTTTCTCTA GAGTTCTCT AGGAAATAG AAAAATAG AAAAATAG AAAAATAG AAAAATAG AAAAATAG AAAAATAG
3801 TAATCAGTGA GGCACCTATC TCAGGATCT GTCTATTTC GTCTATTTC GTCTATTTC GTCTATTTC GTCTATTTC GTCTATTTC GTCTATTTC GTCTATTTC
3901 ATTAGTCACT CCGTGGATAG AGTCCGCTAG CAGATAAAG CAGATAAAG CAGATAAAG CAGATAAAG CAGATAAAG CAGATAAAG CAGATAAAG CAGATAAAG
4001 ATCTGGCCCC AGTGTGCAA TGATACCGG AGACCCAGC TGATACCGG TGATACCGG TGATACCGG TGATACCGG TGATACCGG TGATACCGG TGATACCGG
4101 TAGACCGGGG TCAGACGCTT ACTATGGCG TCTGGTGGC TCTGGTGGC TCTGGTGGC TCTGGTGGC TCTGGTGGC TCTGGTGGC TCTGGTGGC TCTGGTGGC
4201 GGCTCTGCAA CTTTATCCG CTCCATCCG TCTATTAAT TCTATTAAT TCTATTAAT TCTATTAAT TCTATTAAT TCTATTAAT TCTATTAAT TCTATTAAT

FIGURE 5 CONT.

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3401 CCAGGACGTT GAAATAGGCG GAGGTAGGTC AGATAATTAA CAACGGCCCT TCGATCTCAT TCATCAAGCG GTCAATTATC AAACGCGTTG CAACAACGGT
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG
AACGATGTCC GTAGCACCCAC AGTGGAGCA CCAACCATTA CCGAAGTAAG TCGAGGCCAA GGGTTGCTAG CCCGCTCAA TGTACTAGGG GTACAACAC
CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC GATCGTTGTC AGAAGTAAGT TGGCGCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
GTTTTTCGC CAATCGAGGA AGCCAGGAGG CTAGCAACAG TCTTCATTCA ACCGCGTCA CAATAGTGAG TACCAATACC GTCGTGACGT ATTAAGAGAA
ACTGTCAATG CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCAATC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG
TGACAGTACG GTAGGCATTC TACGAAAGA CACTGACCAC TCATGAGTTG GTTCAGTAAG ACTCTATCA CATAGCCCGC TGGCTCAACG AGAACGGGCC
CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA AACGTTCTTC GGGCGGAAA CTCTCAAGGA TCTTACCGCT
GCAGTTATGC CCTATTATGG CGCGGTGTAT CGTCTGAAA TTTTCACGAG TAGTAACCTT TTGCAAGAAG CCCCCTTTT GAGAGTTCCCT AGAATGGCGA
GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTCAACCAGC GTTCTGGGT GAGCAAAAAC AGGAAGGCAA
CAACTCTAGG TCAAGCTACA TTGGGTGAGC ACGTGGTTG ACTAGAGTC GTAGAAAATG AAAGTGGTGC CAAAGACCCA CTCGTTTTTG TCCTTCCGTT
AATGCCGCAA AAAAGGGAAT AAGGCGACA CGGAATGTT GAATACTCAT ACTCTCCTT TTTCAATATT ATTGAAGCAT TTATCTAGAG GTTATTGTCT
TTACGGCGTT TTTTCCCTTA TTCCCGCTGT GCCTTACAA CTTATGAGTA TGAGAAGGA AAAGTTATAA TNACTTCGTA AATAGATCTC CAATAACAGA

3501

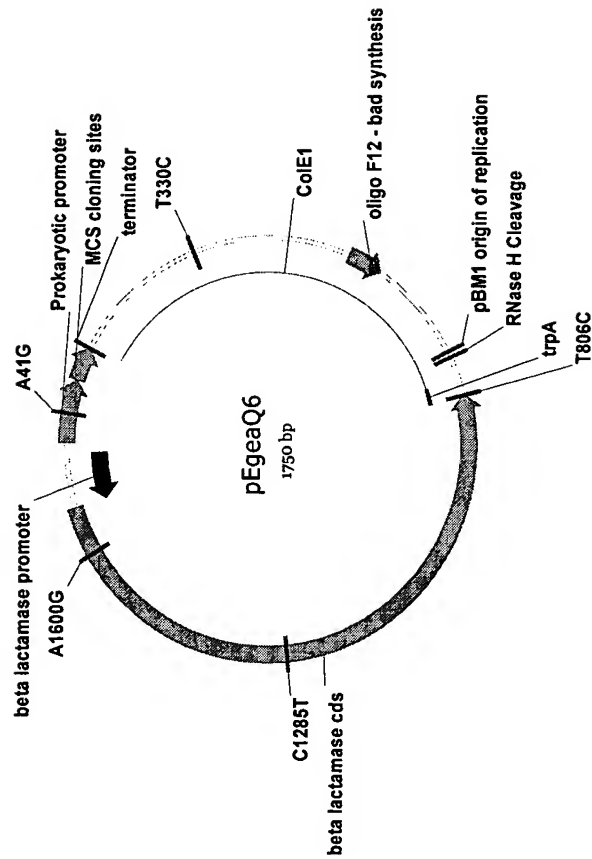
3601

3701

3801

3901

FIGURE 5 CONT.



1 AGTGCTCTAG ACCTGTTGAC AATTAATCAT CGGCTCGTAT AATGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGGATCG ATCGAATTCG
101 TCACGAGATC TGGACAACTG TTAATTAGTA GCCGAGCATA TTACACACCT TAACACTCGC CTATTGTAA AGTGTGTCTT TTGTCTTAGC TAGCTTAAGC
GATCCAAGCT TGAGCTCGAG CCATGGCCCG GGTACCGGCG CCACTTAATA ATCTTTCTA GTTTCCTAGA AGAACTCTAG GAAAAAAGA CGCGCATTAG ACGACGAACG
201 CTAGTTGCGA ACTCGAGCTC GGTACCGGCG CCACTTAATA ATCTTTCTA GTTTCCTAGA AGAACTCTAG GAAAAAAGA CGCGCATTAG ACGACGAACG
AAACAAAAA ACCACGCTA CCAGCGGTGG TTGTGTTGCC GCATCAAGAG CTACCAACTC TTTTCCGAA GGTAACTGGC TTTCAGCAGAG CGCAGATACC
TTTGTTTTTT TGGTGGCGAT GGTGCGCAC AAACAAACGG CCTAGTTCTC GATGTTGAG AAAAAGGCTT CCAATTGACG AAGTCGTCTC GCCTCTATGG
301 AAATACTGTT CTCTTAGTGT AGCCGTAGTT AGGCCACAC TTCAAGAACT CTGTAGCACC GCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT
TTTATGACAA GAAGATCACA TCGGCATCAA TCCGGTGGTG AAGTTCTTGA GACATCTGG CGGATGTATG GAGCGAGAGC ATTAGGACAA TGGTCACCGA
401 GCTGCCAGTG GCGATAAGTC GTGTCTTACC GGTGTTGACT CAAGACGATA GTTACCGGAT AAGCGCGAGC GGTGCGGCTG AACGGGGGT TCGTGCACAC
CGACGGTCAC CGCTATTTCAG CACAGAAATGG CCCAACTGA GTTCTGCTAT CAATGGCTTA TTCCGCGTCG CCAGCCCCGAC TTGCCCCCCA AGCAGCTGTG
501 AGCCGAGCTT GGAGCGAACG ACCTACACCG AACTAGATA CCTACAGCGT GAGCTATGAG AAGCGCCAC GCTTCCGAA GGTACAAAGG CGGACAGGTA
TCGGGTCGAA CCTCGTTTGC TGGATGTGGC TTGACTCTAT GGATGTCGA CTCGATACTC TTTCGCGGTG CGAAAGGCTT CCCTGTTTCC GCCTGTCCAT
601 TCCGTTAAGC GGCAGGGTTC GAACAGAGA GCGCACGAG GAGCTTCCAG GGGGAACGC CTGGAATCTT TATAGTCTG TCGGGTTTCG CCACCTCTGA
AGGCCATTTC GATTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGAA AACCGCCAGC AACCGGCTT TTTACGGTT CTGCCCCGT CATTAGCGCG
701 CTTGAGCGTG GATTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGAA AACCGCCAGC AACCGGCTT TTTACGGTT CTGCCCCGT CATTAGCGCG
GAACTGCGAG CTAAACAC TACGAGCAG CTATCTCAGC GATCTGCTA TTTCGTTTCAT CCATAGTTCG CTGACTCCCC GTGCTGTAGA TAATACGAT
801 GCTATTACCA ATGCTTAATC AGTGAGGCAT TCACCTCCGT GATAGAGTCG CTAGACAGAT AAAGCAAGTA GGTATCGAG GACTGAGGG CAGCACATCT AATTGATGCTA
901 ACGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC CAGCTCACC GGCTCCAGAT TTATCAGCAA TAAACAGCC AGCGGGAAGG
TGCCCTCCCG AATGTFAGAC CGGGGTCAAC ACCTTACTAT GCGCTCTGCG GTGCGAGTGG CCGAGGTCTA AATAGTCTGT ATTGTGTCGG TCGGCCCTTCC

FIGURE 6

1001 GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCTCCA TCCAGTCTAT TAATGTGTC CGGAAGCTA GAGTAAGTAG TTCCGCAAGT AATAGTTGC
CGGCTCGCGT CTTCAACAGG ACGTTGAAAT AGGCGAGGT AGGTGAGATA ATTAACAACG GCCCTTCGAT CTCATTCAATC AAGCGTCAA TTATCAAACG
1101 GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTCACG CTCGTGCTTT GGTATGGCTT CATTGAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG
CGTTGCAACA ACGGTAACGA TGTCGTAGC ACCACATGC GAGCAGCAA GTAAGTCGAG GCAAGGGTT GCCAAGGGTT GCTAGTCCG CTCAATGTAC
1201 ATCCCCCATG TTGTGCAAAA AAGCGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TTGTCAGAAC GCAAGGGTT CACTGTGTTAT TATGCGAGCA
TAGGGGTAC AACACGTTTT TTCGCCAATC GAGGAAGCCA GGAGGTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT
1301 CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC ACCACTCATG TCAACCAAGT CATTCTGAGA ATAGTGATG CGGCGACCGA
GACGTATTAA GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG AACTTAAAG TGCTCATCAT GTAAGACTCT TATCACATAC GCCGTGGCT
1401 GTTGCTCTTG CCCGGGTCA ATACGGGATA ATACCGGCC ACATAGCAGA ACTTTAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGC GAAAACCTCTC
CAACAGAAAC GGGCGCGAGT TATGCCCTAT TATGCGCGG TGTATCGTCT TGAATTTTC ACGTAGTA ACCTTTGA AGAAGCCCCG CTTTGTAGAG
1501 AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCTC CCAACTGATC TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA
TTCTTAGAAT GCGGACAACT CTAGGTCAAG CTACATGGG TGAGCACGAG GGTGACTAG AAGTCGTAGA AAATGAAAGT GGTGCAAG ACCCACTCGT
1601 AAAACAGGAA GGCAAAATGC CGCAAAAAG GGAATAAGG CGACAGGAA ATGTTGAATA CTCATCTCT TCCTTTTCA ATATTATGA AGCATTATC
TTTTGTCCTT CCGTTTACG GCGTTTTC CCTTATCCC GCTGTCCCTT TACAACCTTAT GAGTATGAGA AGGAAGAAAGT TATAATACT TCGTAATAG
1701 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT CTAGAGGTA
TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA GATCTTCCAT

FIGURE 6 CONT.